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OM protein - protein search, using sw model

Run on: March 12, 2002, 12:53:40 ; Search time 12.94 Seconds

(without alignments)  
28,444 Million cell updates/sec

Title: US-09-801-784-36  
Perfect score: 50  
Sequence: 1 PSAAVATYSP 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 4664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : SWISSPROT\_39:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	44	88.0	171	1	FMS1_ECOLI
2	40	80.0	170	1	FMS1_ECOLI
3	36	72.0	234	1	P27411 rabbit hemo
4	36	72.0	326	1	MTC2_CHEV1
5	36	72.0	377	1	VMAT_PIZIT
6	36	72.0	2344	1	POLN_RHIV
7	35	70.0	374	1	ADH7_HUMAN
8	35	70.0	374	1	ADH7_MOUSE
9	35	70.0	486	1	RTG3_YEAST
10	35	70.0	845	1	KRHH_DROME
11	35	70.0	963	1	CHS2_YEAST
12	34	68.0	540	1	ANPC_HUMAN
13	34	68.0	684	1	BL14_CAEEL
14	34	68.0	736	1	IVL2_MOUSE
15	34	68.0	2016	1	CIN5_HUMAN
16	34.5	67.0	291	1	PKRD_SOLAC
17	33	66.0	314	1	GBLP_SCHPO
18	33	66.0	369	1	VMAT_PIZIT
19	33	66.0	375	1	ADH7_HUMAN
20	33	66.0	486	1	RTG3_YEAST
21	33	66.0	438	1	FE1A_DESM
22	33	66.0	547	1	FBI1_ADPAO
23	33	66.0	561	1	ATKA_ANAST
24	33	66.0	664	1	PTSA_STRMO
25	33	66.0	680	1	PAW1_HUMAN
26	33	66.0	919	1	PAW2_HUMAN
27	33	66.0	1274	1	SRE3_BACSU
28	33	66.0	1901	1	AKI1_HUMAN
29	32	64.0	123	1	SDIS_MOUSE
30	32	64.0	169	1	CH21_LJOMI
31	32	64.0	252	1	RTG3_MOUSE
32	32	64.0	307	1	Y172_ARCFU
33	32	64.0	326	1	Y800_PYPAB

## ALIGNMENTS

RESULT 1  
FMS1\_ECOLI STANDARD: 171 AA.  
AC P257401  
DE 01-MAY-1992 (Ref. 22, Created)  
DI 01-MAY-1992 (Ref. 22, Last sequence update)  
DI 01-OCT-1996 (Ref. 44, Last annotation update)  
DE CSI\_FIMBRIAL\_SEGUNIT\_A\_PRECURSOR (CSI\_PILIN).  
CN CSQA OR CSQA.  
OS Escherichia coli.  
OG Plasmid pHE24, and plasmid pHE05.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_Taxid 562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN ENTEROGENOTYPIC / SEROTYPE O15:H28; PLASMID pHE24;  
RX MEDLINE 9135744; PubMed 1679404;  
RA Jordi B.A.M., van Vliet A.H.M., Willems G.A.,  
RT van der Zeijst B.A.M., Gaastria W.;  
RT "Analysis of the first two genes of the CSI fimbrial operon in human  
enterotoxigenic Escherichia coli of serotype O15:H28".  
RT FEMS Microbiol. Lett. 64:265-270(1991).  
RL [2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SEROTYPE O6:H16; PLASMID-P60605;  
RX MEDLINE-9104170; PubMed=1977705;  
RA Perez-Casal J., Searley J.S., Scott J.K.;  
RT "Gene encoding the major subunit of CSI pilin of human enterotoxigenic  
Escherichia coli".  
RT Infect. Immun. 58:3594-3600(1990).  
RL [3]  
RN [3]  
RP SEQUENCE OF 24-42.  
RC MEDLINE-90046745; PubMed 2572584;  
RX Hall R.H., Manaval D.R., Collins J.H., Theibert J.L.,  
RA Levine M.M.;  
RT "Purification and analysis of colonization factor antigen 1, a heat  
surface antigen 1, and coli surface antigen 3 fimbriae from  
enterotoxigenic Escherichia coli".  
RT J. Bacteriol. 171:6372-6374(1989).  
RL [4]  
RN [4]  
RP FUNCTION: FIMBRIAL (ALSO CALLED PIL1), POLAR FILAMENTS BA:ZANT  
FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5  
MICROMETERS AND NUMBERING 100-400 PER CELL. ENABLING BACTERIA TO  
COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.  
-1- INDUCTION: CSI FIMBRIAL ARE ONLY EXPRESSED IN THE PRESENCE OF THE  
POSITIVE REGULATOR RNS.  
-1- SIMILARITY: TO THE CFA/I FIMBRIAL SUBUNIT B (CFAB).  
-1- This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL databank. It is  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
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or send an email to [license@1stb.ch](mailto:license@1stb.ch).



Query Match 72.0% Score 36; DB 1; Length 244;  
 Best Local Similarity 60.0% Pred. No. 6.5;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10  
 1:1:11111  
 DB 84 PNASATITYP 94

RESULT 4  
 MTC2.CHVP1 STANDARD; PRT: 326 AA.  
 AC P11118: Q84569;  
 DT 01-01-1993 (Ref. 26, Created)  
 DT 15-DEC-1998 (Ref. 37, Last sequence update)  
 DT 20-AUG-2001 (Ref. 40, Last annotation update)  
 DE MODIFICATION METHYLASE CVIAT1 (EC 2.1.1.72) (ADENINE SPECIFIC  
 METHYLTRANSFERASE CVIAT1) (M.CVIAT1).  
 CVIAT1 OR A251K.  
 Parametium butsaria chlorolla virus 1 (PhiV-1).  
 Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.  
 NCBI\_TaxID:10506;  
 RX MEDLINE:93065201; PubMed:1437552;  
 RA Zhang Y., Nelson M., Nettlecid J.W., Jarbank D.E., van Etten J.L.;  
 RT "Characterization of Chlorella virus PhiV-1 CVIAT1 restriction and  
 modification system."  
 RL Nucleic Acids Res. 20:5351-5356(1992).  
 RN 121  
 RP REVISIONS AND SEQUENCE FROM N.A.  
 RA MEDLINE:95133167; PubMed:7831789;  
 RA Lu Z., Li Y., Zhang Y., Kotish G.F., Rock D.L., van Etten J.L.;  
 RT "Analysis of 45 kb of DNA located at the left end of the Chlorella  
 virus PhiV-1 genome."  
 RL Virology 206:339-352(1995).  
 CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE  
 CATG, CAUSES SPECIFIC METHYLATION ON A-2 ON BOTH STRANDS AND  
 PROTECTS THE DNA FROM CLEAVAGE BY THE CVIAT1 END-NUCLEASE.  
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE =  
 S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOURINE.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: M86639; AAB92181.1; -;  
 DR EMBL: 042580; AAC96619.1; -;  
 DR PIR: S27901; S27901.  
 DR PIR: S35442; S35442.  
 DR REFSEQ: J5402; M.CVIAT1.  
 DR InterPro: IPR002294; D12N6\_mltase.  
 DR InterPro: IPR002052; No\_MLase.  
 DR Pfam: PF02086; MethyltransID12; 1.  
 DR PRINTS: PR00505; D12N6MTFRASE.  
 DR PROSITE: PS00092; No\_MLASE; 1.  
 KW Transposase; Methyltransferase; Restriction system.  
 SO SEQUENCE 126 AA; 37492 MW; 8C16C75D85F0D89 CRC64;

Query Match 72.0% Score 36; DB 1; Length 126;  
 Best Local Similarity 70.0% Pred. No. 9.3;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10  
 1:1:11111  
 DB 95 JGFFVITVSP 104

RESULT 5  
 VMA1\_P12HT STANDARD; PRT: 377 AA.  
 ID VMA1\_P12HT  
 AC P24266;  
 DT 01-MAR-1992 (Ref. 21, Created)  
 DT 01-MAR-1992 (Ref. 21, Last sequence update)  
 DT 01-AUG-1992 (Ref. 24, Last annotation update)  
 DE MATRIX PROTEIN (MEMBRANE PROTEIN).  
 GN M.  
 OS Human parainfluenza 2 virus (strain Joshiba) (PIV 2).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.  
 NCBI\_TaxID:11214;  
 RX MEDLINE:91049454; PubMed:2173264;  
 RA Kawano M., Bando H., Ohamoto S., Okamoto K., Kondo K., Iseki M.,  
 KA Nishio M., Ito Y.;  
 RT "Complete nucleotide sequence of the matrix gene of human  
 parainfluenza type 2 virus and expression of the M protein in  
 bacteria."  
 RL Virology 179:857-861(1990).  
 CC -1- FUNCTION: THE M PROTEIN HAS A CRUCIAL ROLE IN VIRUS ASSEMBLY  
 AND INTERACTS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL  
 MEMBRANE.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: M62734; AAA46862.1; -;  
 DR EMBL: X57559; CAA40785.1; -;  
 DR PIR: A36421; MENZP2.  
 DR PIR: S16661; S16661.  
 DR InterPro: IPR000982; Matrix.  
 DR Pfam: PF00661; Matrix; 1.  
 DR Prodom: Pro00741; Matrix; 1.  
 KW Matrix protein; Envelope protein.  
 SO SEQUENCE 377 AA; 42412 MW; A181A79C55276746 CRC64;

Query Match 72.0% Score 36; DB 1; Length 377;  
 Best Local Similarity 60.0% Pred. No. 11;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10  
 1:1:11111  
 DB 170 PLEVSITVSP 179

RESULT 6  
 POLN\_RHIV STANDARD; PRT: 244 AA.  
 ID POLN\_RHIV  
 AC P27410;  
 DT 01-AUG-1992 (Ref. 23, Created)  
 DT 01-AUG-1992 (Ref. 23, Last sequence update)  
 DT 20-AUG-2001 (Ref. 40, Last annotation update)  
 DE NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE  
 (EC 2.7.7.48); HELIX PROTEINASE P40 (EC 3.4.22. 2); HELICASE (EC 3.6.1.18)  
 PROTEIN]; CAP PROTEIN].  
 DE Rabbit hemorrhagic disease virus (RHDV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 OC Calicivirus.  
 NCBI\_TaxID:11976;  
 RX MEDLINE:91361557; PubMed:1840711;  
 RA MEDLINE:91361557; PubMed:1840711;

BA Meyer's G., Withlitch C., Thiel H. J.,  
 B1 "Rabbit hemolymphatic disease virus: molecular cloning and nucleotide  
 B2 sequencing of a calicivirus genome." *J. Virol.* 64(1991).  
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DE ALDH6-ALDEHYDE DEHYDROGENASE CLASS IV (EC 1.1.1.1) (RETINOL DEHYDROGENASE)  
DE (CASTROR ALDH6 OR ALDH 4)  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euarchonta; Rodentia; Sciurumorphi; Muridae; Murinae; Mus;  
OX NCBI\_TaxID:10090;  
RN 111  
RP SEQUENCE FROM N.A.  
RC STRAIN FVB/N: TISSUE Gastro mucosa;  
RX MEDLINE 95256259; PubMed 7748026;  
RA Zdobych-Kielbaso M., Ang H.L., Foalot M.H., Duester G.;  
RA Duester G.;  
RT "Gene structure and promoter for Adh 4 encoding mouse class IV alcohol  
RT dehydrogenase (retinol dehydrogenase)".  
RL J. Biol. Chem. 270:10868-10877(1995).  
RN 121  
RP SEQUENCE FROM N.A.  
RC STRAIN C29/SVJ;  
RX MEDLINE 97271564; PubMed 9126489;  
RA Zdobych-Kielbaso M., Duester G., Baschbeck R.J., Foalot M.H.;  
RA Duester G.;  
RT "Gene structure and promoter for Adh 4 encoding mouse class IV alcohol  
RT dehydrogenase (retinol dehydrogenase)".  
RL Genomics 41:105-109(1997).  
CC -1- FUNCTION: COULD FUNCTION IN RETINOL OXIDATION FOR THE SYNTHESIS OF  
CC RETINYLIC ACID, A HIGHLY IMPORTANT FOR CELLULAR DIFFERENTIATION.  
CC -1- CATALYTIC ACTIVITY: Alcohol + NAD(+) = Aldehyde or ketone + NADH.  
CC -1- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE STOMACH MUSCLE, LOW  
CC EXPRESSION IN LIVER, THYMUS, SKIN AND OVARY. VERY LOW EXPRESSION IN  
CC SMALL INTESTINE, LIVER AND UTERUS.  
CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE  
CC FAMILY, CLASS-IV SUBFAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC

DH EMBL: 020257; AAA6745.1;  
DH EMBL: 076744; AA553124.1;  
DH EMBL: 076728; AA553124.1;  
DH EMBL: 076729; AA553124.1;  
DH EMBL: 076740; AA553124.1;  
DH EMBL: 076727; AA553124.1;  
DH EMBL: 076741; AA553124.1;  
DH EMBL: 076743; AA553124.1;  
DH EMBL: 076742; AA553124.1;  
DH MGDB: 0618792; Adh4;  
DH InterPro: IPR002428; Adh\_zinc;  
DH InterPro: IPR02085; Adh\_zinc;  
DH Pfam: PF01107; adh\_zinc\_1;  
DH PROSITE: PS00659; Adh\_ZINC\_1;  
KM oxidoreductase Zinc\_NAD; Multidomain family;  
ET METAL 47 47 ZINC (CATALYTIC) (BY SIMILARITY);  
ET METAL 68 68 ZINC (CATALYTIC) (BY SIMILARITY);  
ET METAL 98 98 ZINC (SECONDARY) (BY SIMILARITY);  
ET METAL 104 104 ZINC (SECONDARY) (BY SIMILARITY);  
ET METAL 104 104 ZINC (SECONDARY) (BY SIMILARITY);  
ET METAL 112 112 ZINC (SECONDARY) (BY SIMILARITY);  
ET METAL 174 174 ZINC (CATALYTIC) (BY SIMILARITY);  
SO SEQUENCE c74 AA: 49847 MW: 6E097BBD4E02D027 CHEM44;

Query Match 70.0% Score 45 DB 1: GenBank c74;  
Best Local Similarity 70.0% Prod. No. 17;  
Matches 72 Conserved type 0 Missed residues 42 Indels 0 Gap 0

111  
SEQUENCE FROM N.A.  
STRAIN GREEN:  
MEDLINE 9718446; PubMed 964248;  
Jha Y., Redwood B., Thornton J., Brown P.A.:  
"A basic helix loop helix leucine zipper transcription complex in  
yeast functions in a stabilizing pathway from mitochondria to the  
nucleus.";  
Mol. Cell. Biol. 17:1110-1117(1997).  
121  
SEQUENCE FROM N.A.  
STRAIN S2000:  
MEDLINE 9607664; PubMed 7502386;  
Chen H., Gassendy J., Fikavand E., Pandey H.:  
"Sequence analysis of a 78.6 kb segment of the left end of  
Yeast 11:1104-1112(1995).  
131  
EXPRESSION: TRANSCRIPTION FACTOR THAT REGULATES CIZ GENE  
EXPRESSION, BINDS TO TWO IDENTICAL SITES ORIENTED AS INVERTED  
REPEATS 28 BP APART IN A REGULATORY UPSTREAM ACTIVATION SEQUENCE  
ELEMENT (QASR) IN THE CIZ PROMOTER. THE CORE BINDING SITE IS 5'-  
GTTTAT-3'.  
141  
SUBUNIT: BINDS TO DNA AS A HETERODIMER WITH RCH.  
151  
SUBCELLULAR LOCATION: NUCLEAR (CYTOSOL) FAMILY OF  
161  
SIMILARITY: BELONGS TO THE BASIC HELIX LOOP HELIX (BHLH) FAMILY OF  
171  
TRANSCRIPTION FACTORS.  
181  
CAUTION: SEE 2 SEQUENCE DIFFERS FROM THAT SHOWN AND IS SHORTER  
(316 AA) DUE TO A FRAMESHIFT.  
191  
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modified and this statement is not removed. Usage by and for commercial  
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or send an email to [license@isb.slb.ch](mailto:license@isb.slb.ch)).

EMBL: U66012; AAA66442.1; ATL FRAME.  
EMBL: X79489; GAA55992.1; ATL FRAME.  
EMBL: Z5864; GAA6429.1; -  
PIR: S45392; S45392.  
BSP: P25012; HELX.  
SDD: S000199; K703.  
InterPro: IPR004015; HLH\_MyC.  
InterPro: IPR010942; HLH\_dlm.  
PIR: P00010; HLH\_1.  
SMART: SM0043; HLH\_1.  
Prosite: PS00048; HLH1\_Loop\_HLH1; 1.  
Transcription regulation: DNA binding: Nuclear protein.  
TNA BIND: 283 296 BASIC DOMAIN.  
TNA BIND: 283 296 BASIC DOMAIN.  
TNA BIND: 283 296 BASIC DOMAIN.  
SEQUENCE: 480 AA; 5419 MW; 106607674001 CpG4;

transcription factor (entry 117).  
Eukaryotic: Metazoa: Artiodactyla: Tragelapha: Bovidae: Insecta:  
Proctoptera: Megoptera: Eudopterygota: Diptera: Brachycera: Musciformia:  
Epithorax: Insectifera: Insectifera:  
MUSCULIN 7227;  
111  
SEQUENCE FROM N.A. (CYTOSOLIC, AND ALTERNATIVE SPLICING).  
STRAIN GREEN-R: TISSUE Embryo, Larva, and Pupae;  
MEDLINE 20287577; PubMed 1072791;  
Focussio P., Jock V., Ruiz C., Richards G.:  
"Regulated heterodimeric a steroid specific modulation of the proopoid oxytocin  
response" is essential for trophoblast metamorphosis.";  
Dev. Biol. 221:33-47(2000).  
121  
SEQUENCE FROM N.A. (ALPHA AND BETA ISOPROTEINS).  
STRAIN BECKLEY:  
MEDLINE 20190000; PubMed 10741182;  
Adams M.D., Schiller S.E., Holt R.A., Evans C.A., Groppe J.D.,  
Aburatani F., Scher S.E., Li P.W., Hoskins R.A., Galle R.E.,  
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
Sutton G.V., Mortier J.R., Yandell M.D., Zhang Q., Chen L.X.,  
Burton R.C., Rogers Y.H., Blazek R.G., Champo M., Pothier B.D.,  
Wan K.H., Boyle C., Baxter E., Holt R.A., Nelson C.K., McKillop G.,  
Mull J.E., Ashburner A., An H., Andrews P., Planchet C., Ralston D.,  
Baker R.M., Bush A., Bakardale J., Bayraktaroglu L., Bosley E.M.,  
Boeson K.Y., Boeson P.V., Berman B.P., Blundell D., Bolshakov S.,  
Botkova D., Botkova M.R., Bouck J., Brackstein P., Brackstein P.,  
Burtis K.C., Busan D.A., Butler H., Cadogan P., Centor A., Chandra L.,  
Cherry J.M., Crawley S., Dahlke C., Davignon L.H., Davies P.,  
de Pablo P., Delcher A., Deng Z., Mays A.J., Jew T., Dietz S.M.,  
Jensen K., Jupp L.E., Jones M., Duran R., Kotha S., Dinkov R.C., Dunn P.,  
Dorbin K.L., Evans-Latta C.C., Ferraz C., Ferreira S., Fleischmann W.,  
Forster C., Gaborillon A.E., Garg N.S., Gelbart W.M., Glasser K.,  
Glocke A., Gong F., Groll J.H., Gu Z., Han P., Harter M.,  
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hock J.,  
Hostin D., Houston K.A., Howland T.J., Wei M.H., Thompson C.,  
Jalili M., Kishish F., Karpov G.H., Ke Z., Kinnison J.A., Kitchin K.A.,  
Kimmel B.E., Kishish F., Kraft C., Kravitz S., Kulp D., Lai Z.,  
Lasko T., Lee Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
Liu X., Maitre B., McIntosh T.C., McLeod M.P., McPherson D.,  
McKulov G., Milshina N.V., Mobarry C., Morris J., Moshir A.,  
Mount S.M., May M., Murphy B., Murphy L., Muzly D.M., Nelson D.L.,  
Nelson D.R., Nelson K.A., Nixon K., Nusskorn D.R., Pachet J.M.,  
Palazzo M., Pattison G.S., Pan S., Pollard J., Pout V., Reese M.A.,  
Reinert M., Remington K., Saunders R.D., Scheibel F., Shen H.,  
Shih K.C., Sides Kiamos L., Simpson M., Skrocki R., Smith L.,  
Soyet E., Spradling A.C., Stapleton M., Strong R., Sun F.,  
Svetskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wong Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
Williams S.M., Woodard J., Wolley K.C., Wu D., Yang S., Yao G.A.,  
Ye J., Yeh R., Zavori J.S., Zhan M., Zhan M., Zhao G., Zhao L.,  
Zhao X.H., Zhang F.N., Zhang W., Zhou G., Zhou S., Zhu X., Smith H.,  
Childs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
\*The genome sequence of trophoblast melanoblasts.\*;  
Science 287:2186-2195(2000).

RN [1]  
 RP MEDLINE=87051757; PubMed=4096579;  
 RA Schib R., Alcher W., Gall U., Goto S., Preiss A., Mair B.,  
 RA Seifert E., Nuber U., Schroeder G., Komler R., Jackle H.;  
 RT \*A conserved family of nuclear proteins containing structural  
 RT elements of the finger protein encoded by Kruppel, a Drosophila  
 RT segmentation gene.\*  
 RL Cell 47:1025-1032(1996).  
 CC  
 CC -1- FUNCTION: PLAYS A GENERAL ROLE IN THE HIERARCHIES OF GENE  
 CC EXPRESSION LEADING TO METAMORPHOSIS.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DEVELOPMENTAL STAGE: BETA ISOFORM IS EXPRESSED DURING  
 CC EMBRYOGENESIS, MOST ABUNDANT IN MIDEKTOGENESIS, AND IN ADULTS.  
 CC ALPHA ISOFORM IS EXPRESSED FROM EMBRYOGENESIS TO 8 HOURS AFTER  
 CC POPULATION. MAJOR PERIOD OF EXPRESSION IS DURING SECOND INSTAR.  
 CC -1- SIMILARITY: BELONGS TO THE KROEPEL FAMILY OF C2H2 TYPE ZINC-  
 CC FINGER PROTEINS.  
 CC  
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 CC  
 CC EMBL: AJ005440; CA006543.2;  
 CC EMBL: AJ005441; CA006544.2;  
 CC EMBL: AF003612; AAF52434.2;  
 CC EMBL: AF003612; AAG22417.1;  
 CC EMBL: M14940; AAA28660.1;  
 CC HSP: P08047; ISP2.  
 CC FLYBASE: FBgn0028420; K1-b1.  
 CC InterPro: IPR000822; Znf-C2H2.  
 CC Pfam: PF00096; Zf-C2H2; 10.  
 CC SMART: SM00355; Znf-C2H2; 8.  
 CC PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 8.  
 CC PROSITE: PS00157; ZINC\_FINGER\_C2H2\_2; 2.  
 CC  
 CC ZINC-finger: Metal-binding; DNA-binding; Repeat: Alternative splicing;  
 CC Developmental protein.  
 CC KW DOMAIN 108 148 GIN RICH.  
 CC FT DOMAIN 482 515 SER/THR-RICH.  
 CC FT DOMAIN 538 565 SER/THR-RICH.  
 CC FT DOMAIN 194 463 ZINC-FINGERS.  
 CC FT ZN\_FING 194 216 C2H2-TYPE.  
 CC FT ZN\_FING 293 293 C2H2-TYPE.  
 CC FT ZN\_FING 299 321 C2H2-TYPE.  
 CC FT ZN\_FING 327 349 C2H2-TYPE.  
 CC FT ZN\_FING 355 377 C2H2-TYPE.  
 CC FT ZN\_FING 383 407 C2H2-TYPE.  
 CC FT ZN\_FING 413 435 C2H2-TYPE.  
 CC FT ZN\_FING 441 463 C2H2-TYPE.  
 CC FT VARSPLIC 1 54 MISSING (IN ISOFORM ALPHA).  
 CC FT CONFLICT 313 413 N > D (IN REF. 3).  
 CC SO SEQUENCE 845 AA; 91451 MW; A41878E98F8E472 C6764;

DT 01-JAN-1990 (Ref. 13, last sequence update)  
 DT 01-MAY-2000 (Ref. 49, last annotation update)  
 DE CHITIN SYNTHASE 2 (EC 2.4.1.16) (CHITIN UDP ACETYL GLUCOSAMINE  
 DE TRANSFERASE 2)  
 GN CHS2 OR YBR048W OR YBR047.  
 OS Saccharomyces cerevisiae (baker's yeast).  
 OC Eukaryota; Euk: Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetaceae; Saccharomycetaceae; Saccharomyces.  
 OC MGI\_taxid 4942;  
 RN [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 9014137; PubMed 2534436;  
 RA Silverman S.J.;  
 RT \*Similar and different domains of chitin synthases 1 and 2 of S.  
 RT cerevisiae: two isozymes with distinct functions.\*  
 RL Yeast 5:459-467(1989).  
 RN [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN S288C;  
 RA Andre B., Czapluch C., Hehn C., Janniaux J.C., Drouotard A.,  
 RA Vissers S.;  
 RL Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP MUTAGENESIS.  
 RA MEDLINE 95294998; PubMed 7775457;  
 RA Nishikawa S., Sudoh M., Ono N., Sawada R., Yamaguchi K., Ichida Y.,  
 RA Mio T., Takai M., Arisawa M., Yamada-Otake H.;  
 RT \*Characterization of chitin synthase 2 of Saccharomyces cerevisiae,  
 RT implication of two highly conserved domains as possible catalytic  
 RT sites.\*  
 RL J. Biol. Chem. 270:13961-13967(1995).  
 CC  
 CC -1- FUNCTION: ESSENTIAL FOR SEPTUM FORMATION AND CELL DIVISION. CHS2  
 CC IS REQUIRED FOR MAINTAINING NORMAL CELL MORPHOLOGY.  
 CC -1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + 11,4-DN-ACETYL-  
 CC BETA-D-GLUCOSAMINYL[(N)-1] -> UDP + 11,4-DN-ACETYL-DETA D-  
 CC GLUCOSAMINYL[(N)-1].  
 CC -1- ENZYME REGULATION: REQUIRES PROTEOLYTIC ACTIVATION.  
 CC -1- SUBCELLULAR LOCATION: INTERNAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.  
 CC  
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 CC  
 CC EMBL: M24865; AAA34493.1;  
 CC EMBL: Z35907; CAAR4980.1;  
 CC PIR: S45167; S45167.  
 CC PIR: A09922; A09922.  
 CC SCD: S0010242; CHS2.  
 CC InterPro: IPR002923; Chitin\_synth.  
 CC InterPro: IPR001173; Glycosyltransf\_2.  
 CC Pfam: PF01644; Chitin\_synth\_1.  
 CC PRODOM: P0002998; Chitin\_synth\_1.  
 CC  
 CC KW Transferrase; glycosyltransferase; Cell wall;  
 CC Multi-subunit family;  
 CC FT DOMAIN 1 422 EXTRA-CELLULAR (POTENTIAL).  
 CC FT TRANSMEM 423 443 1 (POTENTIAL).  
 CC FT DOMAIN 444 643 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 644 664 2 (POTENTIAL).  
 CC FT DOMAIN 665 677 EXTRA-CELLULAR (POTENTIAL).  
 CC FT TRANSMEM 678 698 3 (POTENTIAL).  
 CC FT DOMAIN 699 711 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 712 732 4 (POTENTIAL).  
 CC FT DOMAIN 733 743 EXTRA-CELLULAR (POTENTIAL).  
 CC FT TRANSMEM 744 764 5 (POTENTIAL).  
 CC FT DOMAIN 765 775 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 776 796 6 (POTENTIAL).  
 CC FT DOMAIN 797 875 EXTRA-CELLULAR (POTENTIAL).  
 CC FT TRANSMEM 876 896 7 (POTENTIAL).

PT	TRANSMEM	997	965	908	926	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963	963
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[illegible]







CC -1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.  
 CC -1- SIMILARITY: CONTAINS 1 TO DOMAIN.  
 CC -1- DATABASE: NAME: LQTSdb; NOTE: SCNA mutations page:  
 CC WWW: <http://www.sst.dk/en/torsknud/lqtsdb/scna.htm>.  
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 CC EMBL: M77335; AAA58644.1; -  
 CC MIM: 600163; -  
 DR InterPro: IPR002111; Cat\_channel\_Trip.  
 DR InterPro: IPR000636; Cat\_ion\_chan\_ion\_11q.  
 DR InterPro: IPR001682; Channel\_pore\_ca\_Na.  
 DR InterPro: IPR000048; IQ.  
 DR InterPro: IPR001696; Na\_channel.  
 DR Pfam: PF00520; Ion\_trans; 4.  
 DR Pfam: PF00612; IQ; 1.  
 DR PRINTS: PR00170; NaCHANNEL.  
 DR SMART: SM00015; IQ; 1.  
 DR GlycoProfile: Transmembrane; Ion transport; Voltage-gated channel;  
 KW Glycoprotein; Repeat; Multigene family; Phosphorylation;  
 KW Polymorphism; Disease mutation; Long QT syndrome.  
 FT TRANSMM 127 150 S1 OF REPEAT 1 (POTENTIAL).  
 FT TRANSMM 159 178 S2 OF REPEAT 1 (POTENTIAL).  
 FT TRANSMM 192 210 S3 OF REPEAT 1 (POTENTIAL).  
 FT TRANSMM 217 236 S4 OF REPEAT 1 (POTENTIAL).  
 FT TRANSMM 253 276 S5 OF REPEAT 1 (POTENTIAL).  
 FT TRANSMM 390 415 S6 OF REPEAT 1 (POTENTIAL).  
 FT TRANSMM 712 736 S1 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 748 771 S2 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 780 799 S3 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 806 825 S4 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 842 862 S5 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 914 939 S6 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 1201 1224 S1 OF REPEAT 111 (POTENTIAL).  
 FT TRANSMM 1238 1263 S2 OF REPEAT 111 (POTENTIAL).  
 FT TRANSMM 1291 1317 S3 OF REPEAT 111 (POTENTIAL).  
 FT TRANSMM 1337 1359 S4 OF REPEAT 111 (POTENTIAL).  
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 FT TRANSMM 1444 1470 S6 OF REPEAT 111 (POTENTIAL).  
 FT TRANSMM 1524 1547 S1 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 1559 1582 S2 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 1589 1612 S3 OF REPEAT 11 (POTENTIAL).  
 FT TRANSMM 1623 1644 S4 OF REPEAT 11 (POTENTIAL).  
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 FT CARBOHYD 841 841 N-LINKED (GLCNAC; -) (POTENTIAL).  
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 FT CARBOHYD 1774 1774 N-LINKED (GLCNAC; -) (POTENTIAL).  
 FT CARBOHYD 1955 1955 N-LINKED (GLCNAC; -) (POTENTIAL).  
 FT VARIANT 558 558 H -> R.  
 /FTID\_VAR\_008955.

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FT				/FTID VAR_009455.
FT	VARIANT	1404	1404	T - M (IN LQTS)
FT				/FTID VAR_008956.
FT	VARIANT	1425	1425	N - S (IN LQTS)
FT				/FTID VAR_001577.

Query Motif: 68.98; Score: 34; DB: 1; Length: 2070;  
 Best Local Similarity: 60.08; Pred. No. 1.6e+02;  
 Matches: 6; Conservative: 1; Mismatches: 4; Indels: 0; Gaps: 0;  
 QY 1 PSVALIYSP 10  
 DB 1002 PSVALIYSP 1011

Search completed: March 12, 2002, 12:53:41  
 Job time: 406 sec

